

Please amend the following claims:

12. (Amended) A diagnostic testing method comprising the steps of:

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- (i) providing a sample;
 - (ii) contacting said sample with antisera specific for a Ho-Hi-Ho epitope of contiguous amino acid residues from a polypeptide wherein said epitope is characterized by a hydrophobic-hydrophilic -hydrophobic motif having an optimal length of amino acid residues determined by a method comprising the steps of:
 - a) assigning an average hydropathy value to each amino acid of a polypeptide;
 - b) generating a hydrophilicity plot using the average hydropathy value of each amino acid;
 - c) fitting a curve segment of the hydrophilicity plot to a negative cosine function, wherein a specific period number value of the negative cosine function equates to the number of amino acids in the curve segment, the period number increasing within a predetermined chosen period number range after each sequential lagging through the hydrophilicity plot thereby providing fit-correlation values for each curve segment across the linear sequence when using the specific period number value;
 - d) generating a potential Ho-Hi-Ho epitope set for each specific period number value within the chosen period number range, wherein each potential Ho-Hi-Ho epitope set contains potential Ho-Hi-Ho epitopes that have a fit-correlation value;

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- e) ranking each potential Ho-Hi-Ho epitope in the potential Ho-Hi-Ho epitope set according to positive fit-correlation values wherein the epitope having highest positive-fit correlation value is ranked number one thereby providing ranked Ho-Hi-Ho potential epitopes for each specific period number value;
 - f) examining the positioning of at least the highest ranked Ho-Hi-Ho potential epitopes of each set relative to the linear sequence of the plot of step (a) to determine at least one set of Ho-Hi-Ho potential epitopes that exhibit alternating positioning about an equilibrium position wherein the ranking values of the Ho-Hi-Ho potential epitopes coverage towards or diverge away from the equilibrium position; and
 - g) designating the Ho-Hi-Ho potential epitopes of the set having the most alternating ranking values that converge or diverge as the immunologically active epitopes which have an optimal length equating to numeric value of amino acid residues in the potential epitopes; and
- (iii) detecting the binding of said antisera to a polypeptide in said sample.

19. (Amended) A diagnostic testing method comprising the steps of:

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- (i) providing a sample;
 - (ii) contacting said sample with antisera specific for a Ho-Hi-Ho epitope of contiguous amino acid residues from a polypeptide wherein said epitope is characterized by a hydrophobic-hydrophilic-hydrophobic motif having optimal length of amino acid residues determined a method comprising the steps of:
 - (a) fitting a hydrophilicity and/or hydrophobicity plot generated for the amino acid linear

sequence of a polypeptide to a mathematically generated continuous curve thereby generating potential epitope sets which include ranked potential epitopes having a specific number of amino acid residues, the mathematically generated curve having at least a maximum positive value;

- (b) positioning the ranked potential epitopes for each set on the hydrophilicity and/or hydrophobicity plot to determine the oscillating behavior of the numeric values of ranked potential epitopes; and
- (c) deeming the potential epitopes that exhibit the most alternating position about an equilibrium position when juxtaposed on the hydrophilicity and/or hydrophobicity plot as the theoretical epitopes and their optimal length corresponds to the specific number of amino acid residues in the set of ranked potential epitomes; and

- (iii) detecting the binding of said antisera to a polypeptide in said sample.

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